A modeling approach for a class of static nonlinear systems

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Received 23 November 2014, www.cmnt.lv

Abstract

As the first step of any system analysis, modeling is an important task in scientific studies field. The mathematical modeling has a long research history. However, nonlinear system modeling has still not been well solved. System identification is the theory and methods of establishing mathematical models of systems. In this paper, by using a hybrid technique, a novel identification method for a wide class of static nonlinear system with unknown structure is proposed. The basic idea is as follows. Firstly, the proposed method employs a system model composed with classical models so as to transform the system structure identification problem into a combinatorial optimization problem. Then, the bacterial foraging optimization algorithm is adopted to synchronously implement the identification on the system's structure and parameters. Finally, compared with the existing method in simulation experiments, some examples are given to illustrate the validity of the proposed method.

Keywords: nonlinear system, modeling, identification, classical model, optimization algorithm

1 Introduction

Building models of reality is a central topic in many disciplines of engineering and science. Models can be used for simulations, analysis of the system's behavior and for a better understanding of the underlying physical mechanisms in the system. System identification is the theory and methods of establishing mathematical models of systems. As one of the key issues of system and control science, system identification has been widely applied to the design and analysis of control system. Consequently, system identification becomes one of the current very active subjects, attracting a large number of scientific and technical personnel for their theoretical study to examine the practical problems in different application possibilities [1,2].

Most control systems encountered in practice are nonlinear to some extent, and, although it may be possible to represent systems which are perturbed over a restricted operating range by a linear model, in general, nonlinear processes can only be adequately characterized by a nonlinear model. Since a mathematical description of a process is often a prerequisite to analysis and controller design, the study of system identification techniques has become an established branch of control theory. However, whereas system identification techniques for linear systems are now well established and have been widely applied, the identification of nonlinear systems has not been received such attention. This can, of course, be attributed to the inherent complexity of nonlinear systems and the difficulty of deriving identification algorithms that can be applied to a reasonably large class of nonlinear systems. At present, the identification of nonlinear system is the main topics in the current international identification fields [3-10].

When we have a lot of input–output data from the observation of the identified system, and we have no other information about the system, how to establish the model of the identified system becomes an important issue. Up to now, most existing identification methods have generally resolved some problem of the specific structure in a way [11,12], whilst it can not completely solve system identification problem of which the structure and parameters are completely unknown. To overcome this problem, this note presents a novel identification method for nonlinear system with unknown structure only on the basis of sample data.

In recent years, a new and rapidly growing bacterial foraging optimization algorithm [13] developed by Passion in 2002 has emerged a novel modern search algorithm based on the behaviour of Escherichia coli bacteria. The bacterial foraging optimization algorithm has been tested on many unconstrained global optimization functions like Sphere function, Ackley function and Griewank function, etc. Now, the bacterial foraging optimization algorithm has been successfully applied in many areas [14-19]. Of course, it also provides an important approach for nonlinear system identification.

The contribution of this paper is to synchronously obtain the model of a static nonlinear system with only one record of measured input/output data. Briefly, this paper is organized as follows. Section 2 describes identification problem formulation. Nonlinear system model are obtained based on the bacterial foraging optimization algorithm in Section 3. The selection criterion of meta model is given in Section 4. Section 5 provides some

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simulation examples to illustrate the validity of presented approach. Finally, we offer some concluding remarks in Section 6.

2 Problem description

In this paper, the special idea of the discussed system identification is as follows. Selecting a combination of sub-models is applied to optimally fit sample data among numerous sub-models initially. And then, the parameters of the model are obtained via the following bacterial foraging optimization algorithm.

Here, a kind of multi-input single-output static nonlinear system is considered below. Let y is an observed system output variable, and the input variables x_1, x_2, …, x_m are likely to influence the system. So n groups of sample data, which obtained from the system, can be described as:

$$(y_i, x_{1i}, x_{2i}, \cdots, x_{ji}, \cdots, x_{mi}), \quad (1)$$

where, x_{ji} denotes the j-th sample datum of the i-th group of sample; y_i expresses the output value of the i-th group of sample; j=1,2,…,m ; i=1,2,…,n.

Assume that the obtained model from sample data is a sample data model; and such model is structured by the mutual superposition of all possible sub-models, as well as the sub-model is consisted of meta model (i.e., classical mathematical model).

Definition 1. There is a single variable x_i, and it takes $f(x_i)$ as form to influence the output of the system, so the $f(x_i)$ is called a single variable meta model.

Assuming the number of single variable meta model is N_1, from Definition 1, considering each input variable may be influence the output of the system via all possible model forms. Then, sample data model can be expressed as:

$$y = p_0 + \sum_{k=1}^{N_1}\sum_{i=1}^{m} f_k(x_i), \quad (2)$$

where, p_0 is a constant term. It can be seen that the above mentioned sample data model is structured by the mutual combination of $N_1 \times m$ meta models.

Definition 2. There are two variables x_i and x_j, and they take $f(x_i, x_j)$, $x_i \neq x_j$ as form to influence the output of the system, moreover, the $f(x_i, x_j)$ can not be decomposed into the form $f(x_i)+f(x_j)$. So the $f(x_i, x_j)$ is called a two variables meta model.

Assuming the number of two variables meta model is N_2, from Definitions 1 and 2, considering each input variable may be combine by various possible model forms. Therefore, sample data model can be described as:

$$y = p_0 + \sum_{k=1}^{N_1}\sum_{i=1}^{m} f_k(x_i) + \sum_{k=1}^{N_2}\sum_{i=1}^{m}\sum_{\substack{j=1 \\ j\neq i}}^{m} f_k(x_i, x_j). \quad (3)$$

We can see that the sample data model is composed of the mutual combination of $N_1 \times m + N_2 \times m \times (m\text{-}1)$ meta models.

In summary, the general form of the sample data model can always be described as:

$$y = p_0 + \sum_{k=1}^{N_1} M_k(x, p_{k,1}, p_{k,2}, \cdots, p_{k,mk}), \quad (4)$$

where, p_0 is a constant term. N is the number of sub-model. $M_k(x, p_{k,1}, p_{k,2}, \ldots, p_{k,mk})$ is the k-th sub-model which is constituted by the meta model and its independent variables, where x can denote either single variable or multiple variables, k=1, 2,…, N. mk is the parameter number. $p_{k,mj}$ is the j-th parameter, j=1, 2, …, mk.

Because the sub-model can take many forms, it may be either linear or nonlinear. Thereby, the parameters of the model are not identical along with the different sub-model. Up to now, to our best knowledge, there is not a feasible and effective identification method for such problem in existing literature. Consequently, studying such problem has a certain practical significance. Generally, the purpose of system identification is that the system outputs $y(t)$ can be best approximated the known system outputs $y_0(t)$. Thereby, we may minimize the following cost function:

$$J = \sum_{t}[y(t) - y_0(t)]^2. \quad (5)$$

Because minimizing Equation (5) is an optimization problem, the minimal value of Equation (5) and the corresponding minimal value point can be obtained by the following bacterial foraging optimization algorithm. Accordingly, we simultaneously achieve the identification for the structure and parameters of nonlinear system.

3 Constructing system model process

In this paper, the proposed system identification method can be divided into the selection of the sub-model (namely, structure identification of the system) problem and the parameter identification problem of the system model.

Selecting sub-model from multitudinous sub-models, which can be best fit sample data, belongs to a class of combinatorial optimization problem, and that the structure of a set of selected mathematical model is unknown. Thereby, there is no conventional method to identify model's parameters. Moreover, the parameter identification problem also belongs to a nonlinear optimization problem. Consequently, we employ the following bacterial foraging optimization algorithm to solve such optimization problem in this paper. The optimization in bacterial foraging optimization comprises the following processes [13].

a) Chemotaxis: This process simulates the movements of an Escherichia coli cell through swimming and tumbling via flagella. Biologically, an Escherichia coli bacterium can move in two different ways. It can swim for a period of time in the same direction or it may tumble, and alternate between these two modes of operation for the entire lifetime. Suppose $\theta^i(j, k, l)$ is i-th bacterium at j-th chemotactic, k-th reproductive and l-th elimination dispersal step. $C(i)$ is the size of the step taken in the

random direction specified by the tumble. Then in computational chemotaxis the movement of the bacterium may be represented by:

$$\theta^i(j+1,k,l)=\theta^i(j,k,l)+C(i)\frac{\Delta(i)}{\sqrt{\Delta^{\mathrm{T}}(i)\Delta(i)}}, \quad (6)$$

where Δ is not unitary, and it is normalized before use it $\mathbf{\Delta}(i)/\sqrt{\mathbf{\Delta}^{\mathrm{T}}(i)\mathbf{\Delta}(i)}$.

b) Swarming: Interesting group behaviour has been observed for several motile species of bacteria including Escherichia coli and salmonella typhimurium, where stable spatio-temporal patterns (swarms) are formed in semisolid nutrient medium. A group of Escherichia coli cells arrange themselves in a traveling ring by moving up the nutrient gradient when placed amidst a semisolid matrix with a single nutrient chemo-effecter. The cells when stimulated by high level of succinate release an attractant aspartate, which helps them to aggregate into groups and thus move as concentric patterns of swarms of high bacterial density. The cell to cell, signaling in Escherichia coli swarm may be represented with the function.

c) Reproduction: After chemotactic steps, the fitness values for the *i*-th bacterium in the chemotaxis loop are calculated by:

$$J^i_{\mathrm{health}}=\sum_{j=1}^{N_c+1}J(i,j,k,l), \quad (7)$$

where J^i_{health} represents the health of the *i*-th bacterium. The smaller the J^i_{health} is the healthier the bacterium is. To simulate the reproduction character in nature and to accelerate the swarming speed, all the bacteria are sorted according to their health values in an ascending order and each of the first bacteria splits into two bacteria. The characters including location and step length of the mother bacterium are reproduced to the children bacteria. Through this selection process the remaining unhealthier bacteria are eliminated and discarded. To simplify the algorithm, the number of the bacteria keeps constant in the whole process.

d) Elimination–dispersal: For the purpose of improving the global search ability, elimination–dispersal event is defined after reproductive steps. The bacteria are eliminated and dispersed to random positions in the optimization domain according to the elimination–dispersal probability. This elimination–dispersal event helps the bacterium avoid being trapped into local optima.

The pseudo code of the bacterial foraging optimization algorithm can be written as follows.

Step 1. Initialize parameters: n, N, N_C, N_S, N_{re}, N_{ed}, P_{ed}, $C(i)$ (i=1, 2, … , N). Where n: dimension of the search space (namely, number of parameters to be optimized), N: the number of bacteria in the population, N_C: chemotactic steps, N_S: swim length, N_{re}: the number of reproduction steps, N_{ed}: the number of elimination–dispersal events, P_{ed}: elimination–dispersal with probability, $C(i)$: the size of the step taken in the random direction specified by tumble.

Step 2. Elimination–dispersal loop: $l = l + 1$

Step 3. Reproduction loop: $k = k + 1$

Step 4. Chemotaxis loop: $j = j + 1$

Step 4.1. For i=1, 2, … , N, take a chemotactic step for bacterium i as follows.

Step 4.2. Compute fitness function, $J(i, j, k, l)$ (in this paper, Equation (5) is taken as the fitness function $J(i, j, k, l)$). Let, $J(i, j, k, l) = J(i, j, k, l) + J_{cc}(\theta^i(j, k, l), P(j, k, l))$, where

$$J_{cc}(\theta,P(j,k,l))=\sum_{i=1}^{N}J_{cc}(\theta,\theta^i(j,k,l))=$$
$$\sum_{i=1}^{N}[d_{\mathrm{attractant}}\exp(-w_{\mathrm{attractant}}\sum_{m=1}^{n}(\theta_m-\theta_m^i)]^2)+ \quad (8)$$
$$\sum_{i=1}^{N}[h_{\mathrm{repellant}}\exp(-w_{\mathrm{repellant}}\sum_{m=1}^{n}(\theta_m-\theta_m^i)]^2),$$

where $J_{cc}(\theta, P(j, k, l))$ is the objective function value to be added to the actual objective function to present a time varying objective function. $\theta=[\theta_1, \theta_2,\ldots, \theta_n]^{\mathrm{T}}$ is a point in the n-dimensional search domain. $P(j, k, l)=\{\theta^i(j, k, l) \mid i=1, 2, \ldots, N\}$ is the set of the bacterial swarm foraging position. $d_{\mathrm{attractant}}$ is the depth of the attractant released by the cell. $w_{\mathrm{attractant}}$ is a measure of the width of the attractant signal. $h_{\mathrm{repellant}}$ is the height of the repellant effect (magnitude) and $w_{\mathrm{repellant}}$ is a measure of the width of the repellant.

Step 4.3. Let $J_{\mathrm{last}} = J(i, j, k, l)$ to save this value since a better cost via a run.

Step 4.4. Tumble: generate a random vector $\Delta(i)\in R^n$ with $\Delta_m(i)$, m=1, 2, …, n, a random number on [-1, 1].

Step 4.5. Move: let $\theta^i(j+1,k,l)=\theta^i(j,k,l)+C(i)(\Delta(i)/\sqrt{\Delta^{\mathrm{T}}(i)\Delta(i)})$, this results in a step of size $C(i)$ in the direction of the tumble for bacterium i.

Step 4.6. Compute $J(i, j, k, l)$ and let $J(i, j, k, l) = J(i, j, k, l) + J_{cc}(\theta^i(j, k, l), P(j, k, l))$.

Step 4.7. Swim

{1} Let $m = 0$ (counter for swim length).

{2} while $m < N_S$ (if have not climbed down too long).

• Let $m = m + 1$

• If $J(i, j + 1, k, l) < J_{\mathrm{last}}$, let $J_{\mathrm{last}} = J(i, j + 1, k, l)$ and let $\theta^i(j+1,k,l)=\theta^i(j,k,l)+C(i)(\Delta(i)/\sqrt{\Delta^{\mathrm{T}}(i)\Delta(i)})$ and use this $\theta^i(j + 1, k, l)$ to compute the new $J(i, j + 1, k, l)$ as in Substep 6.

• Else, let $m = N_S$. This is the end of the while statement.

Step 4.8. Go to next bacterium (i+1) if $i \neq N$ (i.e., go to Substep 2 to process the next bacterium).

Step 5. If $J < N_C$, go to Step 4. In this case, continue chemotaxis, since the life of the bacteria is not over.

Step 6. Reproduction

• For the given k and l, and for each i=1, 2, … , N, let $J_{\text{health}}^{i}=\sum_{j=1}^{N_C+1}J(i,j,k,l)$ be the health of the bacterium i. Sort bacteria and chemotactic parameters $C(i)$ in order of ascending cost J_{health} (higher cost means lower health).

• The S_r bacteria with the highest J_{health} values die and the other S_r bacteria with the best values split.

Step 7. If $k < N_{re}$, go to Step 3. In this case, we have not reached the number of specified reproduction steps, so we start the next generation in the chemotactic loop.

Step 8. Elimination–dispersal: for i=1, 2, … , N, with probability P_{ed}, eliminate and disperse each bacterium, and this keeps the number of bacteria in the population constant. To do this, if a bacterium is eliminated, simply disperse one to a random location on the optimization domain.

Step 9. If $l < N_{ed}$, then go to Step 2; otherwise end, Then, optimal value of the objective function J and the corresponding optimal point are obtained.

4 Selecting meta model

Sample data model is composed by the various sub-models, and each sub-model is constituted by the combination of meta models and their independent variables. So the selection of the meta model plays a decisive role in the proposed system identification method. Moreover, the selection of the meta model should abide by the following principles:

1) Common property: It includes usually emergent model in the correlation research field;

2) Typical property: Different models should possess different character;

3) Covering property: It contains as far as possible relation or law by the combination of the meta model.

In the simulation study of this paper, we select the following typical meta model.

i) The linear model: $y=bx$;

ii) The exponential function model: $y=ae^{bx}$;

iii) The power function model: $y=ax^{b}$;

iv) The logarithmic function model: $y=a\ln x$;

v) The hyperbolic function model: $y=a/(b+x)$;

vi) The periodic function model: $y=a\cos(bx+c)$.

5 Simulation examples

In order to illustrate the effectiveness of the proposed identification method, the following examples show the estimation process for nonlinear systems.

BFOA represents the bacterial foraging optimization algorithm; GA stands for the genetic algorithm.

Example 1 Consider the following system:

$$y=0.5x-1.6\cos(0.6x+1)+\frac{0.5}{0.2+x}. \tag{9}$$

According to Equation (9), 50 groups of sample data are generated, but assuming that the structure of the nonlinear system model is not given in advance. Thereby, we select all meta models provided in this paper to implement the identification of the system based on the proposed identification approach. In simulation, the parameters of the above-mentioned BFOA are set: n=6, N=10, N_C =100, N_S =4, N_{re} =4, N_{ed} =2, P_{ed} =0.25, and $C(i)$=0.025.

After multiple simulations are carried out using the BFOA, and the following results are obtained.

$$y=0.0023+0.4988x-1.5896\cos(0.5998x+0.9896)+\frac{0.5017}{0.2003+x}. \tag{10}$$

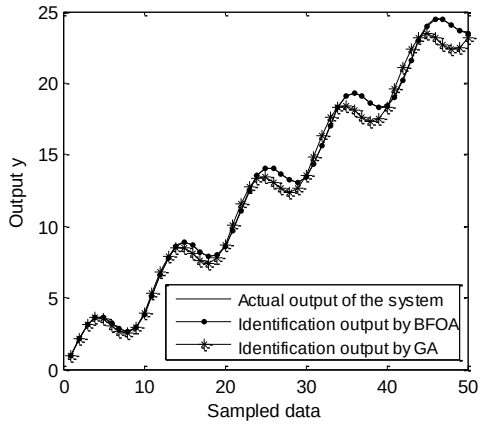

FIGURE 1 Identification results of Example 1

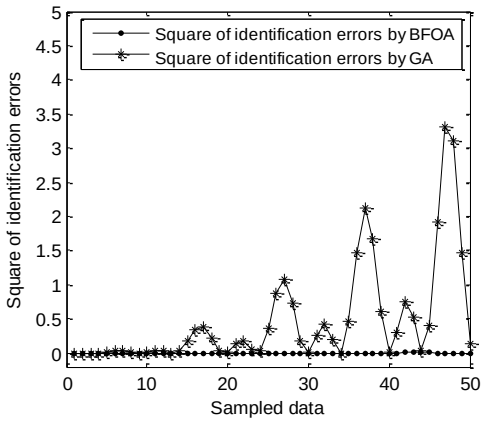

FIGURE 2 Square curves of identification error of Example 1

In order to show the validity of the proposed method, we further adopt the GA [4] to identify the system, and the following results are gotten.

$$y=0.0037+0.4906x-1.6035\cos(0.6201x+0.9645)+\frac{0.4895}{0.1830+x}. \tag{11}$$

Moreover, the maximal deviations of using the BFOA and GA identification are 0.0807 and 1.8189, respectively. The mean square errors are 0.0219 and 0.4736, respectively. And their fitting results are shown in Figure 1, while the curves of their identification error squared are depicted in Figure 2, respectively.

Example 2 In accordance with Equation (9), 50 sets of sample data are also produced. Moreover, the random disturbances are generated on the interval [-10%, +10%] and added to the sample data according to 10%. In this case, we still assume that the structure of the system model is unknown in advance, and select all meta model provided in this paper to implement identification for the system. In simulation, the main parameters of the BFOA are same as those of Example 1. After multiple simulations using the BFOA and the GA are still carried out, we choose the following better identification results, respectively.

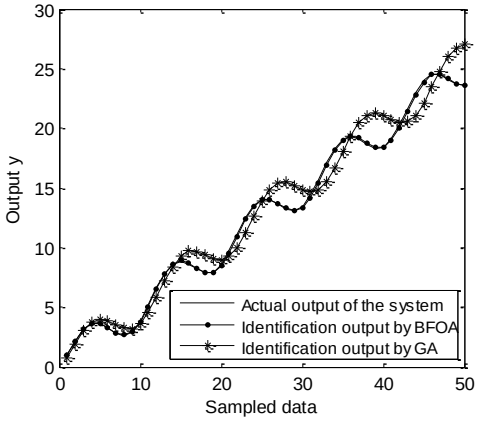

FIGURE 3 Identification results of Example 2

$$y = 0.0095 + 0.4976x - 1.5869\cos(0.5975x + 0.9795) + \frac{0.5110}{0.2044 + x}, \quad (12)$$

$$y = 0.0120 + 0.5131x - 1.5804\cos(0.5586x + 0.8832) + \frac{0.5129}{0.2075 + x}. \quad (13)$$

The maximal deviations of using the BFOA and GA identification are 0.2976 and 3.0772, respectively. Moreover, the mean square errors are 0.0737 and 0.8624, respectively. And the fitting results and identification errors are shown in Figures 3 and 4, respectively.

From the simulation results of the above Examples 1 and 2, when the disturbances appear, the structure and parameters for the nonlinear system can still better identified using the BFOA identification. Thereby, we can see that the proposed identification method is effective and reasonable. That is to say, the presented identification approach can better meet the engineering practical requirement.

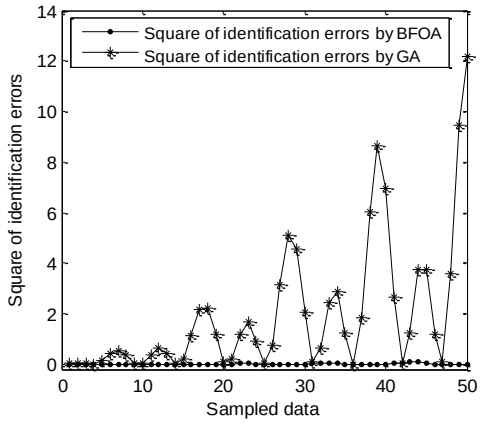

FIGURE 4 Square curves of identification error of Example 2

6 Conclusion

Aim at a class of nonlinear system with unknown structure, a novel identification method of the static nonlinear system is presented. The idea is to employ a system model composed with classical models so as to change the system structure identification problem into a combinational problem initially. And then, the BFOA is applied to carry out the identification of the model parameters. Thus, the structure and parameters of nonlinear system are simultaneously estimated on the basis of sample data. Finally, simulation examples validate that the proposed method can obtain higher accuracy and robustness.

Acknowledgments

This work was supported by the Scientific Research Program Funded by Shaanxi Provincial Education Department of China under Grant No. 14JK1538, the Project Supported by Shaanxi Provincial Natural Science Foundation research of China under Grant No. 2014JM8325, the Doctoral Scientific Research Start-up Funds of Teachers of Xi'an University of Technology of China under Grant No. 108-211006 and the National Natural Science Foundation of China under Grant No. 91120014.

References

[1] Wang L Y, Zhao W X 2013 *Acta Automatica Sinica* **39**(7) 933-42 *(in Chinese)*
[2] Strejc V 1981 *Automatica* **17**(1) 7-21
[3] Giannakis G B, Serpedin E 2001 *Signal Processing* **81**(3) 533-80
[4] Liu S A, Tang F 2007 *System Engineering Theory and Practice* **3**(3) 134-7
[5] Tang Y G, Qiao L J, Guan X P 2010 *Expert Systems with Applications* **37**(10) 3398-404
[6] Spall J C 2014 *IEEE Transactions on Automatic Control* **59**(1) 3-17
[7] Niedźwiecki M, Gackowski S 2013 *IEEE Transactions on Automatic Control* **58**(7) 1847-53
[8] Cai Z J, Bai E W 2012 *IEEE Transactions on Automatic Control* **57**(7) 738-42
[9] Sjöberd J, Schoukens J 2012 *Automatica* **48**(2) 353-9
[10] Giri F, Rochdi Y, Brouri A, Chaoui F Z 2011 *Automatica* **47**(8) 1827-33
[11] Sjöberg J, Zhang Q H, Ljung L, Benveniste A, Delyon B, Glorennec P Y, Hjalmarsson H, Juditsky A 1995 *Automatica* **31**(12) 1691-724
[12] Haastrup M, Hansen M R, Ebbesen M K, Mouritsen O Ø 2012 *Modeling, identification and Control* **33**(1) 1-11
[13] Passino K M 2002 *IEEE Control Systems Magazine* **22**(3) 52-67

[14] Mishra S 2005 *IEEE Transactions on Evolutionary Computation* **9**(1) 61-73
[15] Flah A, Sbita L 2013 *Applied Intelligence* **38**(1) 114-29
[16] Kim D H, Abraham A, Cho J H 2007 *Information Sciences* **117**(18) 3918-37
[17] Bhushan B, Singh M 2011 *Applied Software Computing* **11**(10) 4913-20
[18] Ray P K, Subuhi B 2012 *Applied Software Computing* **12**(6) 1965-77
[19] Lin W X, Liu P X, Li W L, Chen Y H, Ou C 2009 *Journal of System Simulation* **24**(10) 3100-4

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